General information

Entry name	LIP1_CANRU
Accession number	P20261
Created	Rel. 17, 1-FEB-1991
Sequence update	Rel. 27, 1-OCT-1993
Annotation update	Rel. 41, 15-JUN-2002

XP-002230351

Description and origin of the Protein

Description	Lipase 1 precursor (EC 3.1.1.3).
Gene name(s)	LIP1.
Organism source	Candida rugosa (Yeast) (Candida cylindracea).
Taxonomy	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; mitosporic Saccharomycetales; Candida.
NCBI TaxID	5481

References

[1] Longhi,S., Fusetti,F., Grandori,R., Lotti,M., Vanoni,M., Alberghina,L.,
Cloning and nucleotide sequences of two lipase genes from Candida cylindracea.
(1992) *Biochim. Biophys. Acta* **1131**:227-232

> Position SEQUENCE FROM N.A.
> Comments STRAIN=ATCC 14830;
> Medline 92305068
> PubMed 1610906

[2] Kawaguchi,Y., Honda,H., Taniguchi-Morimura,J., Iwasaki,S.,
The codon CUG is read as serine in an asporogenic yeast Candida cylindracea.
(1989) *Nature* **341**:164-166

> Position SEQUENCE OF 12-549 FROM N.A., AND PARTIAL SEQUENCE.
> Comments STRAIN=ATCC 14830 / MS-5;
> Medline 89384874
> PubMed 2506450

[3] Grochulski,P., Li,Y., Schrag,J.D., Bouthillier,F., Smith,P., Harrison,D., Rubin,B., Cygler,M.,
Insights into interfacial activation from an open structure of Candida rugosa lipase.
(1993) *J. Biol. Chem.* **268**:12843-12847

> Position X-RAY CRYSTALLOGRAPHY (2.06 ANGSTROMS).
> Medline 93286131
> PubMed 8509417

[4] Grochulski,P., Bouthillier,F., Kazlauskas,R.J., Serreqi,A.N., Schrag,J.D., Ziomek,E., Cygler,M.,
Analogs of reaction intermediates identify a unique substrate binding site in Candida rugosa lipase.
(1994) *Biochemistry* **33**:3494-3500

> Position X-RAY CRYSTALLOGRAPHY (2.05 ANGSTROMS).
> Medline 94190867
> PubMed 8142346

[5] Benjamin,S., Pandey,A.,
Candida rugosa lipases: molecular biology and versatility in biotechnology.
(1998) *Yeast* **14**:1069-1087

> Position REVIEW.
> Medline 98451816

PubMed 9778794

Comments

CATALYTIC ACTIVITY	TRIACYLGLYCEROL + H(2)O = DIACYLGLYCEROL + A FATTY ACID ANION.
SIMILARITY	BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.

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Database cross-references

EMBL	X64703;CAA45957.1;-.
	X16712;CAA34684.1;-.
PIR	S05684;S05684.
	S23448;S23448.
PDB	1CRL;31-JAN-94.
	1LPM;20-APR-95.
	1LPN;20-APR-95.
	1LPO;20-APR-95.
	1LPP;20-APR-95.
	1LPS;08-MAR-95.
	1TRH;31-JAN-94.
InterPro	IPR002018;CarbesteraseB.
	IPR000379;Ser_estrs_site.
Pfam	PF00135;COesterase;1.
PROSITE	PS00122;CARBOXYLESTERASE_B_1;1.
	PS00941;CARBOXYLESTERASE_B_2;1.

Keywords

Hydrolase; Lipid degradation; Signal; Glycoprotein; Multigene family; 3D-structure;

Features

Key	Begin	End	Length	Description
SIGNAL	1	15	15	
CHAIN	16	549	534	LIPASE 1.
ACT_SITE	224	224	1	
ACT_SITE	356	356	1	
ACT_SITE	464	464	1	
DISULFID	75	112	38	
DISULFID	283	292	10	
CARBOHYD	329	329	1	N-LINKED (GLCNAC...).
CARBOHYD	366	366	1	N-LINKED (GLCNAC...).
VARIANT	398	398	1	G -> Q.

STRAND	18	20	3
TURN	22	23	2
STRAND	26	28	3
STRAND	30	31	2
STRAND	36	42	7
STRAND	44	44	1
HELIX	49	51	3
TURN	52	53	2
STRAND	58	58	1
TURN	64	65	2
STRAND	67	67	1
STRAND	69	69	1
STRAND	74	74	1
TURN	80	81	2
HELIX	88	97	10
TURN	98	98	1
HELIX	100	105	6
STRAND	108	108	1
STRAND	114	119	6
TURN	121	122	2
TURN	125	126	2
STRAND	129	135	7
TURN	139	141	3
TURN	146	147	2
HELIX	151	159	9
TURN	160	161	2
STRAND	165	169	5
HELIX	174	178	5
HELIX	182	187	6
TURN	188	188	1
TURN	190	191	2
HELIX	192	207	16
HELIX	208	211	4
TURN	212	212	1
STRAND	213	223	11
TURN	224	224	1
HELIX	225	235	11
HELIX	236	239	4
STRAND	242	243	2
TURN	244	245	2
STRAND	246	247	2
STRAND	251	255	5
TURN	265	266	2
HELIX	268	281	14

TURN	282	282	1
TURN	284	285	2
HELIX	289	295	7
HELIX	298	306	9
TURN	307	307	1
TURN	311	312	2
TURN	314	317	4
HELIX	334	339	6
TURN	340	341	2
STRAND	348	353	6
TURN	354	354	1
STRAND	355	355	1
TURN	356	357	2
HELIX	358	361	4
HELIX	362	364	3
TURN	365	366	2
HELIX	370	380	11
TURN	382	383	2
HELIX	386	395	10
HELIX	400	402	3
TURN	406	407	2
TURN	409	412	4
HELIX	418	429	12
TURN	430	430	1
HELIX	431	440	10
STRAND	446	451	6
TURN	453	456	4
TURN	458	460	3
STRAND	463	463	1
TURN	464	465	2
HELIX	466	472	7
TURN	473	473	1
TURN	477	478	2
HELIX	479	482	4
TURN	483	483	1
HELIX	484	492	9
HELIX	495	498	4
STRAND	507	507	1
TURN	510	511	2
STRAND	517	520	4
STRAND	525	528	4
HELIX	534	541	8
HELIX	544	547	4

Sequence Information

7-2-200

Length: **549 aa**, molecular weight: **58550 Da**, CRC64 checksum: **27A40BD318757CE0**

```
MELALALSLI ASVAAAPTAT LANGDTITGL NAIINEAFLG IPFAEPPVGN LRFKDPVPYS        60
GSLDGQKFTS YGPSCMQQNP EGTYEENLPK AALDLVMQSK VFEAVSPSSE DCLTINVVRP       120
PGTKAGANLP VMLWIFGGGF EVGGTSTFPP AQMITKSIAM GKPIIHVSVN YRVSSWGFLA       180
GDEIKAEGSA NAGLKDQRLG MQWVADNIAA FGGDPTKVTI FGESAGSMSV MCHILWNDGD       240
NTYKGKPLFR AGIMQSGAMV PSDAVDGIYG NEIFDLLASN AGCGSASDKL ACLRGVSSDT       300
LEDATNNTPG FLAYSSLRLS YLPRPDGVNI TDDMYALVRE GKYANIPVII GDQNDEGTFF       360
GTSSLNVTTD AQAREYFKQS FVHASDAEID TLMTAYPGDI TQGSPFDTGI LNALTPQFKR       420
ISAVLGDLGF TLARRYFLNH YTGGTKYSFL SKQLSGLPVL GTFHSNDIVF QDYLLGSGSL       480
IYNNAFIAFA TDLDPNTAGL LVKWPEYTSS SQSGNNLMMI NALGLYTGKD NFRTAGYDAL       540
FSNPPSFFV                                                              549
//
```

General Description References Comments Links Keywords Features Sequence

Title: EP02009616_0010.PROT
Application Date: 07-Feb-2003

```
>>SWALL:LIP1_CANRU P20261 Lipase 1 precursor (EC 3.1.1.3  (549 aa) 01-Feb-1991
 initn: 3466 init1: 3466 opt: 3468  Z-score: 3919.8  bits: 735.1 E(): 3.8e-210
Smith-Waterman score: 3468;  96.276% identity (96.276% ungapped) in 537 aa overlap (11·
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```
                10        20        30        40        50
EP0200    SMNSRGPAGRLGSVPTATLANGDTITGLNAIINEAFLGIPFAEPPVGNLRFKDPVPYS
                  ...::::::::::::::::::::::::::::::::::::::::::::::::::
SWALL:  MELALALSLIASVAAAPTATLANGDTITGLNAIINEAFLGIPFAEPPVGNLRFKDPVPYS
                10        20        30        40        50        60

          60        70        80        90        100       110
EP0200  GSLDGQKFTSYGPSCMQQNPEGTYEENLPKAALDLVMQSKVFEAVSPSSEDCLTINVVRP
        :::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
SWALL:  GSLDGQKFTSYGPSCMQQNPEGTYEENLPKAALDLVMQSKVFEAVSPSSEDCLTINVVRP
                70        80        90        100       110       120

          120       130       140       150       160       170
EP0200  PGTKAGANLPVMLWIFGGGFEVGGTSTFPPAQMITKSIAMGKPIIHVSVNYRVSSWGFLA
        :::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
SWALL:  PGTKAGANLPVMLWIFGGGFEVGGTSTFPPAQMITKSIAMGKPIIHVSVNYRVSSWGFLA
                130       140       150       160       170       180

          180       190       200       210       220       230
EP0200  GDEIKAEGSANAGLKDQRMGMQWVADNIAAFGGDPTKVTIFGESAGSMSVMCHILWNDGD
        ::::::::::::::::::::::::.::::::::::::::::::::::::::::::::::::
SWALL:  GDEIKAEGSANAGLKDQRLGMQWVADNIAAFGGDPTKVTIFGESAGSMSVMCHILWNDGD
                190       200       210       220       230       240

          240       250       260       270       280       290
EP0200  NTYKGKPLFRAGIMQSGAMVPSDAVDGVYGNEIFDLLASDAGCGSASDKLACLRGVSSDT
        :::::::::::::::::::::::::::::::.::::::::::.::::::::::::::::::
SWALL:  NTYKGKPLFRAGIMQSGAMVPSDAVDGIYGNEIFDLLASNAGCGSASDKLACLRGVSSDT
                250       260       270       280       290       300

          300       310       320       330       340       350
EP0200  LEDATNNTPGFLAYSSLRLSYLPRPDGVNITDDMFALVREGKYASVPVIIGDQNDEGTFF
        :::::::::::::::::::::::::::::::::::.:::::::::::.:::::::::::::
SWALL:  LEDATNNTPGFLAYSSLRLSYLPRPDGVNITDDMYALVREGKYANIPVIIGDQNDEGTFF
                310       320       330       340       350       360

          360       370       380       390       400       410
EP0200  GTSSLNVTTDAEARQYFTQSFVHASDAELDTLMTAYPQDITQGSPFDTGVLNALTPQFKR
        :::::::::::.::.::.: :::::::::::.::::::::: ::::::::::.::::::::
SWALL:  GTSSLNVTTDAQAREYFKQSFVHASDAEIDTLMTAYPGDITQGSPFDTGILNALTPQFKR
                370       380       390       400       410       420

          420       430       440       450       460       470
EP0200  ISAVLGDLAFIHARRYFLNHYTGGTKYSFLSKQLSGLPVLGTFHSNDIVFQDYLLGSGSL
        ::::::::.:  ::::::::::::::::::::::::::::::::::::::::::::::::::
SWALL:  ISAVLGDLGFTLARRYFLNHYTGGTKYSFLSKQLSGLPVLGTFHSNDIVFQDYLLGSGSL
                430       440       450       460       470       480

          480       490       500       510       520       530
EP0200  IYNNAFIAFATDLDPNTAGLLVKWPEYTSSSQSGNNLMMINALGLYTGKDNSRTAGYDAL
        ::::::::::::::::::::::::::::::::::::::::::::::::::: ::::::::::
SWALL:  IYNNAFIAFATDLDPNTAGLLVKWPEYTSSSQSGNNLMMINALGLYTGKDNFRTAGYDAL
                490       500       510       520       530       540

          540
EP0200  FSNPPSFFV
```

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          : : : : : : : : :
SWALL:  FSNPPSFFV
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